

SEQUENCE LISTING

<110> Gross, Jane A.
 Xu, Wenfeng
 Madden, Karen
 Yee, David P.

<120> SOLUBLE RECEPTOR BR43X2 AND METHODS OF USING

<130> 98-75C2

<150> 60/115,068

<151> 1999-01-07

<150> 60/169,890

<151> 1999-12-09

<150> 09/479,856

<151> 2000-01-07

<150> 09/569,245

<151> 2000-05-11

<160> 60

<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (6)...(746)

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Asp	Gln	Glu	Glu	Arg	Trp	Ser	Leu	Ser	Cys	Arg	Lys	Glu	Gln	Gly	Lys	
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00220"9022960

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Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys	
35 40 45	
gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg	194
Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg	
50 55 60	
agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa	242
Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu	
65 70 75	
gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac	290
Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His	
80 85 90 95	
aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca	338
Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala	
100 105 110	
gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt gcc	386
Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala	
115 120 125	
gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag agg	434
Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg	
130 135 140	
ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt ccg	482
Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro	
145 150 155	
gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg agc	530
Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser	
160 165 170 175	
aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag tgc	578
Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys	
180 185 190	
agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac ccc	626
Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro	
195 200 205	
act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag	674

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Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln
 210 215 220

cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct 722
 Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro
 225 230 235

gcc cag gag ggg ggc cca ggt gca taaatggggg tcaggaggagg aaaggaggag 776
 Ala Gln Glu Gly Gly Pro Gly Ala
 240 245

ggagagagat ggagaggagg ggagagagaa agagaggtgg ggagagggga gagagatatg 836
 aggagagaga gacagaggag gcagagaggg agagaaacag aggagacaga gagggagaga 896
 gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaga ggcagagaag 956
 gaaagaggca gagagggaga gaggcagaga gggagagagg cagagagaca gagagggaga 1016
 gagggacaga gagagataga gcaggaggtc ggggcactct gagtcccagt tcccagtga 1076
 gctgtaggtc gtcacacacct aaccacacgt gcaataaagt cctcgtgcct gctgctcaca 1136
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 <212> PRT
 <213> Homo sapiens

<400> 2

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 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
 20 25 30
 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
 35 40 45
 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
 50 55 60
 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
 65 70 75 80
 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
 85 90 95
 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
 100 105 110
 Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val
 115 120 125
 Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly
 130 135 140
 Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala
 145 150 155 160

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Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr
 165 170 175
 Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg
 180 185 190
 Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr
 195 200 205
 Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro
 210 215 220
 Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala
 225 230 235 240
 Gln Glu Gly Gly Pro Gly Ala
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(360)

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 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
 20 25 30

tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt gga 144
 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
 35 40 45

cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc 192
 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
 50 55 60

cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt 240
 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
 65 70 75 80

gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga 288
 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg

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85

90

95

ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca gat 336
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cag gtg gcc ctg gtc tac agc acg 360
 Gln Val Ala Leu Val Tyr Ser Thr
 115 120

<210> 4

<211> 120

<212> PRT

<213> Homo sapiens

<400> 4

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1 5 10 15
 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
 20 25 30
 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
 35 40 45
 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
 50 55 60
 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
 65 70 75 80
 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
 85 90 95
 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
 100 105 110
 Gln Val Ala Leu Val Tyr Ser Thr
 115 120

<210> 5

<211> 1377

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14)...(895)

<400> 5

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Ser	Arg	Val	Asp	Gln	Glu	Glu	Arg	Phe	Pro	Gln	Gly	Leu	Trp	Thr	Gly	
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gtg	gct	atg	aga	tcc	tgc	ccc	gaa	gag	cag	tac	tgg	gat	cct	ctg	ctg	145
Val	Ala	Met	Arg	Ser	Cys	Pro	Glu	Glu	Gln	Tyr	Trp	Asp	Pro	Leu	Leu	
		30				35					40					
ggt	acc	tgc	atg	tcc	tgc	aaa	acc	att	tgc	aac	cat	cag	agc	cag	cgc	193
Gly	Thr	Cys	Met	Ser	Cys	Lys	Thr	Ile	Cys	Asn	His	Gln	Ser	Gln	Arg	
		45			50					55					60	
acc	tgt	gca	gcc	ttc	tgc	agg	tca	ctc	agc	tgc	cgc	aag	gag	caa	ggc	241
Thr	Cys	Ala	Ala	Phe	Cys	Arg	Ser	Leu	Ser	Cys	Arg	Lys	Glu	Gln	Gly	
				65					70					75		
aag	ttc	tat	gac	cat	ctc	ctg	agg	gac	tgc	atc	agc	tgt	gcc	tcc	atc	289
Lys	Phe	Tyr	Asp	His	Leu	Leu	Arg	Asp	Cys	Ile	Ser	Cys	Ala	Ser	Ile	
			80					85					90			
tgt	gga	cag	cac	cct	aag	caa	tgt	gca	tac	ttc	tgt	gag	aac	aag	ctc	337
Cys	Gly	Gln	His	Pro	Lys	Gln	Cys	Ala	Tyr	Phe	Cys	Glu	Asn	Lys	Leu	
		95				100						105				
agg	agc	cca	gtg	aac	ctt	cca	cca	gag	ctc	agg	aga	cag	cgg	agt	gga	385
Arg	Ser	Pro	Val	Asn	Leu	Pro	Pro	Glu	Leu	Arg	Arg	Gln	Arg	Ser	Gly	
		110				115					120					
gaa	gtt	gaa	aac	aat	tca	gac	aac	tcg	gga	agg	tac	caa	gga	ttg	gag	433
Glu	Val	Glu	Asn	Asn	Ser	Asp	Asn	Ser	Gly	Arg	Tyr	Gln	Gly	Leu	Glu	
					130				135						140	
cac	aga	ggc	tca	gaa	gca	agt	cca	gct	ctc	ccg	ggg	ctg	aag	ctg	agt	481
His	Arg	Gly	Ser	Glu	Ala	Ser	Pro	Ala	Leu	Pro	Gly	Leu	Lys	Leu	Ser	
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gca	gat	cag	gtg	gcc	ctg	gtc	tac	agc	acg	ctg	ggg	ctc	tgc	ctg	tgt	529
Ala	Asp	Gln	Val	Ala	Leu	Val	Tyr	Ser	Thr	Leu	Gly	Leu	Cys	Leu	Cys	
			160					165					170			
gcc	gtc	ctc	tgc	tgc	ttc	ctg	gtg	gcg	gtg	gcc	tgc	ttc	ctc	aag	aag	577
Ala	Val	Leu	Cys	Cys	Phe	Leu	Val	Ala	Val	Ala	Cys	Phe	Leu	Lys	Lys	

175	180	185	
agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt			625
Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser			
190	195	200	
ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg			673
Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val			
205	210	215	220
agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag			721
Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu			
	225	230	235
tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac			769
Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp			
	240	245	250
ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg			817
Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu			
	255	260	265
cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg			865
Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val			
	270	275	280
cct gcc cag gag ggg ggc cca ggt gca taa atgggggtca gggagggaaa			915
Pro Ala Gln Glu Gly Gly Pro Gly Ala *			
285	290		
ggaggagggga gagagatgga gaggagggga gagagaaaga gaggtgggga gaggggagag			975
agatatgagg agagagagac agaggaggca gaaagggaga gaaacagagg agacagagag			1035
ggagagagag acagagggag agagagacag aggggaagag aggcagagag ggaaagaggc			1095
agagaaggaa agagacaggc agagaaggag agaggcagag agggagagag gcagagaggg			1155
agagaggcag agagacagag agggagagag ggacagagag agatagagca ggaggtcggg			1215
gcactctgag tcccagttcc cagtgcagct gtaggtcgtc atcacctaac cacacgtgca			1275
ataaagtcct cgtgcctgct gctcacagcc cccgagagcc cctcctcctg gagaataaaa			1335
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<210> 6

<211> 293

<212> PRT

<213> Homo sapiens

<400> 6

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			20					25					30		
Ser	Cys	Pro	Glu	Glu	Gln	Tyr	Trp	Asp	Pro	Leu	Leu	Gly	Thr	Cys	Met
		35					40					45			
Ser	Cys	Lys	Thr	Ile	Cys	Asn	His	Gln	Ser	Gln	Arg	Thr	Cys	Ala	Ala
		50				55					60				
Phe	Cys	Arg	Ser	Leu	Ser	Cys	Arg	Lys	Glu	Gln	Gly	Lys	Phe	Tyr	Asp
65					70					75					80
His	Leu	Leu	Arg	Asp	Cys	Ile	Ser	Cys	Ala	Ser	Ile	Cys	Gly	Gln	His
				85					90					95	
Pro	Lys	Gln	Cys	Ala	Tyr	Phe	Cys	Glu	Asn	Lys	Leu	Arg	Ser	Pro	Val
			100					105					110		
Asn	Leu	Pro	Pro	Glu	Leu	Arg	Arg	Gln	Arg	Ser	Gly	Glu	Val	Glu	Asn
		115					120					125			
Asn	Ser	Asp	Asn	Ser	Gly	Arg	Tyr	Gln	Gly	Leu	Glu	His	Arg	Gly	Ser
		130				135						140			
Glu	Ala	Ser	Pro	Ala	Leu	Pro	Gly	Leu	Lys	Leu	Ser	Ala	Asp	Gln	Val
145					150					155					160
Ala	Leu	Val	Tyr	Ser	Thr	Leu	Gly	Leu	Cys	Leu	Cys	Ala	Val	Leu	Cys
				165					170					175	
Cys	Phe	Leu	Val	Ala	Val	Ala	Cys	Phe	Leu	Lys	Lys	Arg	Gly	Asp	Pro
			180					185					190		
Cys	Ser	Cys	Gln	Pro	Arg	Ser	Arg	Pro	Arg	Gln	Ser	Pro	Ala	Lys	Ser
		195					200					205			
Ser	Gln	Asp	His	Ala	Met	Glu	Ala	Gly	Ser	Pro	Val	Ser	Thr	Ser	Pro
		210				215					220				
Glu	Pro	Val	Glu	Thr	Cys	Ser	Phe	Cys	Phe	Pro	Glu	Cys	Arg	Ala	Pro
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<212> DNA
<213> Homo sapiens
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10 15 20

cct tgt caa ctt cga tgt tct tct aat act cct cct cta aca tgt cag 332
Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln
25 30 35

cgt tat tgt aat gca agt gtg acc aat tca gtg aaa gga acg aat gcg 380
Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Thr Asn Ala
40 45 50

att ctc tgg acc tgt ttg gga ctg agc tta ata att tct ttg gca gtt 428
Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu Ile Ile Ser Leu Ala Val
55 60 65 70

ttc gtg cta atg ttt ttg cta agg aag ata agc tct gaa cca tta aag 476
 Phe Val Leu Met Phe Leu Leu Arg Lys Ile Ser Ser Glu Pro Leu Lys
 75 80 85

gac gag ttt aaa aac aca gga tca ggt ctc ctg ggc atg gct aac att 524
 Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu Leu Gly Met Ala Asn Ile
 90 95 100

gac ctg gaa aag agc agg act ggt gat gaa att att ctt ccg aga ggc 572
 Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu Ile Ile Leu Pro Arg Gly
 105 110 115

ctc gag tac acg gtg gaa gaa tgc acc tgt gaa gac tgc atc aag agc 620
 Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys Glu Asp Cys Ile Lys Ser
 120 125 130

aaa ccg aag gtc gac tct gac cat tgc ttt cca ctc cca gct atg gag 668
 Lys Pro Lys Val Asp Ser Asp His Cys Phe Pro Leu Pro Ala Met Glu
 135 140 145 150

gaa ggc gca acc att ctt gtc acc acg aaa acg aat gac tat tgc aag 716
 Glu Gly Ala Thr Ile Leu Val Thr Thr Lys Thr Asn Asp Tyr Cys Lys
 155 160 165

agc ctg cca gct gct ttg agt gct acg gag ata gag aaa tca att tct 764
 Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu Ile Glu Lys Ser Ile Ser
 170 175 180

gct agg taa ttaaccattt cgactcgagc agtgccactt taaaaatctt 813
 Ala Arg *

ttgtcagaat agatgatgtg tcagatctct ttaggatgac tgtatTTTTc agttgccgat 873
 acagctTTTT gtcctctaac tgtggaaact ctttatgtta gatataTTTc tctaggTTac 933
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<210> 8

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<212> PRT

<213> Homo sapiens

<400> 8

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 Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser
 35 40 45
 Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu
 50 55 60
 Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile
 65 70 75 80
 Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu
 85 90 95
 Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu
 100 105 110
 Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys
 115 120 125
 Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe
 130 135 140
 Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys
 145 150 155 160
 Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu
 165 170 175
 Ile Glu Lys Ser Ile Ser Ala Arg
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<210> 9

<211> 245

<212> PRT

<213> Homo sapiens

<400> 9

Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp Gln Glu Glu Arg
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 20 25 30
 Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met Ser Cys Lys Thr
 35 40 45
 Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala Phe Cys Arg Ser
 50 55 60
 Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp His Leu Leu Arg
 65 70 75 80
 Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His Pro Lys Gln Cys
 85 90 95
 Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val Asn Leu Pro Pro
 100 105 110
 Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn Asn Ser Asp Asn
 115 120 125

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Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser Glu Ala Ser Pro
 130 135 140
 Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val Ala Leu Val Tyr
 145 150 155 160
 Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys Cys Phe Leu Val
 165 170 175
 Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro Cys Ser Cys Gln
 180 185 190
 Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser Ser Gln Asp His
 195 200 205
 Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro Glu Pro Val Glu
 210 215 220
 Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro Thr Gln Glu Ser
 225 230 235 240
 Ala Val Thr Pro Gly
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<210> 10

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Motif describing the cysteine-rich pseudo-repeat domain

<221> VARIANT

<222> (1)...(2)

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<221> VARIANT

<222> (4)...(4)

<223> Xaa is any amino acid residue except cysteine.

<221> VARIANT

<222> (5)...(5)

<223> Xaa is glutamine, glutamic acid, or lysine.

<221> VARIANT

<222> (6)...(6)

<223> Xaa is glutamine, glutamic acid, lysine, asparagine, arginine, aspartic acid, histidine, or serine.

- <221> VARIANT
<222> (7)...(7)
<223> Xaa is glutamine or glutamic acid.
- <221> VARIANT
<222> (8)...(9)
<223> Each Xaa is independently any amino acid residue except cysteine, or absent.
- <221> VARIANT
<222> (10)...(11)
<223> Xaa is tyrosine, phenylalanine, or tryptophan.
- <221> VARIANT
<222> (13)...(13)
<223> Xaa is any amino acid residue except cysteine.
- <221> VARIANT
<222> (16)...(17)
<223> Each Xaa is independently any amino acid residue except cysteine.
- <221> VARIANT
<222> (19)...(19)
<223> Xaa is isoleucine, methionine, leucine, or valine.
- <221> VARIANT
<222> (20)...(20)
<223> Xaa is any amino acid residue except cysteine.
- <221> VARIANT
<222> (22)...(24)
<223> Each Xaa is independently any amino acid residue except cysteine.
- <221> VARIANT
<222> (26)...(31)
<223> Each Xaa is independently any amino acid residue except cysteine.
- <221> VARIANT
<222> (32)...(33)
<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<221> VARIANT

<222> (35)...(36)

<223> Each Xaa is independently any amino acid residue except cysteine.

<221> VARIANT

<222> (37)...(37)

<223> Xaa is tyrosine or phenylalanine.

<221> VARIANT

<222> (39)...(40)

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<400> 10

Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Leu	Leu	Xaa
1			5				10						15		
Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		20					25					30			
Xaa	Cys	Xaa	Xaa	Xaa	Cys	Xaa	Xaa								
		35					40								

<210> 11

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide sequence encoding the polypeptide of SEQ ID NO:4

<221> variation

<222> (1)...(360)

<223> Each N is independently A, T, G, or C.

<400> 11

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tggsnytnw	sntgymgnaa	rgarcarggn	aarttytayg	aycayytnyt	nmngaytg	120
athwsntgyg	cnwsnathtg	yggncarcay	ccnaarcart	gygcntaytt	ytgygaraay	180
aarytnmgw	snccngtnaa	yytnccncn	garytnmgm	gncarmgnws	nggngargtn	240
garaayaayw	sngayaayws	nggnmgntay	carggnytn	arcaymgngg	nwsngargcn	300
wsnccngcny	tnccnggnyt	naarytnwsn	gcngaycarg	tngcnytngt	ntaywsnacb	360

<210> 12

<211> 741
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide sequence encoding a polypeptide of SEQ ID NO:2

<221> variation
 <222> (1)...(741)
 <223> Each N is independently A, T, G, or C.

<400> 12

atgwsnggny tnggmgnws nmgnmgnggn ggnmgwnsm gngtngayca rgargarmgn	60
tggwsnytnw sntgymgnaa rgarcarggn aarttytayg aycayytnyt nmngaytgy	120
athwsntgyg cnwsnathtg yggncarcay ccnaarcart gygcntaytt ytgygaraay	180
aarytnmgmw snccngtnaa yytnccnccn garytnmgm gncarmgnws nggngargtn	240
garaayaayw sngayaayws nggnmgntay carggnytn gncaymgngg nwsngargcn	300
wsnccngcny tnccnggnyt naarytnwsn gcngaycarg tngcnytngt ntaywsnacd	360
ytnggnytn gyytnygygc ngtnytnygy tgyttyytn tngcngtngc ntgyttyytn	420
aaraarmgng gngayccntg ywsntgyar ccnmgnwnsm gncnmgnc rwsnccngcn	480
aarwsnwsnc argaycaygc natggargcn ggnwsnccng tnwsnacd nccngarccn	540
gtngaracnt gywsnttytg yttccngar tgymgngcnc cnacncarga rwsngcngtn	600
acnccnggna cncngaycc nacntgygc gnmngntgg gntgycayac nmgnacnacn	660
gtnytnarc cntgyccnca yathccngay wsnggnytn gnathgtntg ygtncngcn	720
cargarggng gncngngc n	741

<210> 13
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FLAG tag

<400> 13
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 14
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>

09627206 "072700

<223> Glu-Glu tag

<400> 14

Glu Glu Tyr Met Pro Met Glu

1

5

<210> 15

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC19980

<400> 15

cgaagagcag tactgggatc ctct

24

<210> 16

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC19981

<400> 16

gccaaaggcca ctgtctggga tgt

23

<210> 17

<211> 1149

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (236)...(1027)

<400> 17

gaattcggca	cgaggcagaa	aggagaaaat	tcaggataac	tctcctgagg	ggtgagccaa	60
gccctgccat	gtagtgcacg	caggacatca	acaaacacag	ataacaggaa	atgatccatt	120
ccctgtggtc	acttattcta	aaggccccaa	ccttcaaagt	tcaagtagtg	atatggatga	180
ctccacagaa	agggagcagt	cacgccttac	ttcttgccct	aagaaaagag	aagaa atg	238
					Met	
					1	

002220"90222960

aaa ctg aag gag tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct	286
Lys Leu Lys Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser	
5 10 15	
gtc cga tcc tcc aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg	334
Val Arg Ser Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu	
20 25 30	
gca ctg ctg tct tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc	382
Ala Leu Leu Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala	
35 40 45	
gcc ctg caa ggg gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac	430
Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His	
50 55 60 65	
cac gcg gag aag ctg cca gca gga gca gga gcc ccc aag gcc ggc ctg	478
His Ala Glu Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu	
70 75 80	
gag gaa gct cca gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca	526
Glu Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro	
85 90 95	
gct cca gga gaa ggc aac tcc agt cag aac agc aga aat aag cgt gcc	574
Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala	
100 105 110	

007270-072700

gtt cag ggt cca gaa gaa aca gtc act caa gac tgc ttg caa ctg att 622
Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile
115 120 125

gca gac agt gaa aca cca act ata caa aaa gga tct tac aca ttt gtt 670
Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val
130 135 140 145

cca tgg ctt ctc agc ttt aaa agg gga agt gcc cta gaa gaa aaa gag 718
Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu
150 155 160

aat aaa ata ttg gtc aaa gaa act ggt tac ttt ttt ata tat ggt cag 766
Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly Gln
165 170 175

gtt tta tat act gat aag acc tac gcc atg gga cat cta att cag agg 814
Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg
180 185 190

aag aag gtc cat gtc ttt ggg gat gaa ttg agt ctg gtg act ttg ttt 862
Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe
195 200 205

cga tgt att caa aat atg cct gaa aca cta ccc aat aat tcc tgc tat 910
Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys Tyr
210 215 220 225

tca gct ggc att gca aaa ctg gaa gaa gga gat gaa ctc caa ctt gca 958
Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala
230 235 240

ata cca aga gaa aat gca caa ata tca ctg gat gga gat gtc aca ttt 1006
Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr Phe
245 250 255

ttt ggt gca ttg aaa ctg ctg tgacctactt acaccatgtc tgtagctatt 1057
Phe Gly Ala Leu Lys Leu Leu
260

ttcctccctt tctctgtacc tctaagaaga aagaatctaa ctgaaaatac caaaaaaaaa 1117
aaaaaaaaaa aaaaaaccct cgagcggccg cc 1149

<210> 18

<211> 264

09627206.072700

<212> PRT

<213> Homo sapiens

<400> 18

Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro
 1 5 10 15
 Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu
 20 25 30
 Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val
 35 40 45
 Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly
 50 55 60
 His His Ala Glu Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly
 65 70 75 80
 Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro
 85 90 95
 Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg
 100 105 110
 Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu
 115 120 125
 Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe
 130 135 140
 Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys
 145 150 155 160
 Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly
 165 170 175
 Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln
 180 185 190
 Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu
 195 200 205
 Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys
 210 215 220
 Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu
 225 230 235 240
 Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr
 245 250 255
 Phe Phe Gly Ala Leu Lys Leu Leu
 260

<210> 19

<211> 1430

<212> DNA

<213> Mus musculus

<220>

00427206 "072700

<221> CDS

<222> (102)...(848)

<400> 19

ttggcgcagg agcgtgcgta ggattgctcg ctcacaacag gcacctgact ggtattgaaa	60
gccgagtcctt cccttcctct ttaaaggatt ggtgaccagg c atg gct atg gca ttc	116
	Met Ala Met Ala Phe
	1 5

tgc ccc aaa gat cag tac tgg gac tcc tca agg aaa tcc tgt gtc tcc	164
Cys Pro Lys Asp Gln Tyr Trp Asp Ser Ser Arg Lys Ser Cys Val Ser	
	10 15 20

tgt gca ctg acc tgc agc cag agg agc cag cgc acc tgt aca gac ttc	212
Cys Ala Leu Thr Cys Ser Gln Arg Ser Gln Arg Thr Cys Thr Asp Phe	
	25 30 35

tgc aaa ttc atc aat tgc cga aaa gag caa ggc agg tac tac gac cat	260
Cys Lys Phe Ile Asn Cys Arg Lys Glu Gln Gly Arg Tyr Tyr Asp His	
	40 45 50

ctc ctg ggg gcc tgc gtc agc tgt gac tcc acc tgc aca cag cac cct	308
Leu Leu Gly Ala Cys Val Ser Cys Asp Ser Thr Cys Thr Gln His Pro	
	55 60 65

cag cag tgt gcc cac ttc tgt gag aaa agg ccc aga agc cag gcg aac	356
Gln Gln Cys Ala His Phe Cys Glu Lys Arg Pro Arg Ser Gln Ala Asn	
	70 75 80 85

ctc cag ccc gag ctc ggg aga cca cag gcc ggg gag gtg gaa gtc agg	404
Leu Gln Pro Glu Leu Gly Arg Pro Gln Ala Gly Glu Val Glu Val Arg	
	90 95 100

tca gac aac tca gga agg cac cag gga tct gag cat ggt cca gga ttg	452
Ser Asp Asn Ser Gly Arg His Gln Gly Ser Glu His Gly Pro Gly Leu	
	105 110 115

09627206 072700

agg cta agt agc gac cag ctg act ctc tac tgc aca ctg ggg gtc tgc 500
 Arg Leu Ser Ser Asp Gln Leu Thr Leu Tyr Cys Thr Leu Gly Val Cys
 120 125 130

ctc tgc gcc atc ttc tgc tgt ttc ttg gtg gcc ttg gcc tcc ttc ctc 548
 Leu Cys Ala Ile Phe Cys Cys Phe Leu Val Ala Leu Ala Ser Phe Leu
 135 140 145

agg cgt aga gga gag cca cta ccc agc cag cct gcc ggg cca cgt ggg 596
 Arg Arg Arg Gly Glu Pro Leu Pro Ser Gln Pro Ala Gly Pro Arg Gly
 150 155 160 165

tca caa gca aac tct ccc cac gcc cac cgc ccc gtg aca gag gct tgc 644
 Ser Gln Ala Asn Ser Pro His Ala His Arg Pro Val Thr Glu Ala Cys
 170 175 180

gac gag gtg acc gcg tca ccc cag cct gtg gaa acg tgt agc ttc tgc 692
 Asp Glu Val Thr Ala Ser Pro Gln Pro Val Glu Thr Cys Ser Phe Cys
 185 190 195

ttc ccg gag cgc agt tct ccc act cag gag agc gcg ccg cgt tcg ctc 740
 Phe Pro Glu Arg Ser Ser Pro Thr Gln Glu Ser Ala Pro Arg Ser Leu
 200 205 210

ggg ata cac ggc ttc gcg ggc act gcc gcc ccg cag ccc tgt atg cgt 788
 Gly Ile His Gly Phe Ala Gly Thr Ala Ala Pro Gln Pro Cys Met Arg
 215 220 225

gca aca gta ggc ggc ctg ggt gtc ctg cgc gca tcc act ggg gac gct 836
 Ala Thr Val Gly Gly Leu Gly Val Leu Arg Ala Ser Thr Gly Asp Ala
 230 235 240 245

cgt ccg gca act tgacagcccg aaaaataaaa aagacaattt agaggatgga 888
 Arg Pro Ala Thr

gtgacagagg gggaaagga tggagaagag acagatgaag acacgataaa ggaagcccg 948
 ctgcacccac gcagagcaac aaagcaacca cctgcagcgc ccacgttccc agcaccgcct 1008
 gtgcctgccg ctgtgtccta tactttccag agcagtcaac ctgtgccttt tttctttagt 1068
 cgagaaagat ggagaatgac cggcacctag cattaccctt acaattctta caaacaagtg 1128
 gtctttccta tggccttagg cagatagctg agtgcagtgt ggatgtattt gtgatttaag 1188
 taacttgtat gtgtatgtgc agattcgggg ttatgtcata tgtgcatgta tacgtgagtt 1248
 gtgtgtctgt atgagttgtg tgtatatgtg cgcctataaa tatgtgtgtg aattctgtgc 1308
 atgcagatgt gtgtgtacat atgtgtctgg ctgatgtggt atagccagaa agatgagggc 1368
 ccttctaggt gaaggccaaa catctaaaaa ccatctaggt gatgggtgct cgtgccgaat 1428

tc

1430

<210> 20
 <211> 249
 <212> PRT
 <213> Mus musculus

<400> 20

Met Ala Met Ala Phe Cys Pro Lys Asp Gln Tyr Trp Asp Ser Ser Arg
 1 5 10 15
 Lys Ser Cys Val Ser Cys Ala Leu Thr Cys Ser Gln Arg Ser Gln Arg
 20 25 30
 Thr Cys Thr Asp Phe Cys Lys Phe Ile Asn Cys Arg Lys Glu Gln Gly
 35 40 45
 Arg Tyr Tyr Asp His Leu Leu Gly Ala Cys Val Ser Cys Asp Ser Thr
 50 55 60
 Cys Thr Gln His Pro Gln Gln Cys Ala His Phe Cys Glu Lys Arg Pro
 65 70 75 80
 Arg Ser Gln Ala Asn Leu Gln Pro Glu Leu Gly Arg Pro Gln Ala Gly
 85 90 95
 Glu Val Glu Val Arg Ser Asp Asn Ser Gly Arg His Gln Gly Ser Glu
 100 105 110
 His Gly Pro Gly Leu Arg Leu Ser Ser Asp Gln Leu Thr Leu Tyr Cys
 115 120 125
 Thr Leu Gly Val Cys Leu Cys Ala Ile Phe Cys Cys Phe Leu Val Ala
 130 135 140
 Leu Ala Ser Phe Leu Arg Arg Arg Gly Glu Pro Leu Pro Ser Gln Pro
 145 150 155 160
 Ala Gly Pro Arg Gly Ser Gln Ala Asn Ser Pro His Ala His Arg Pro
 165 170 175
 Val Thr Glu Ala Cys Asp Glu Val Thr Ala Ser Pro Gln Pro Val Glu
 180 185 190
 Thr Cys Ser Phe Cys Phe Pro Glu Arg Ser Ser Pro Thr Gln Glu Ser
 195 200 205
 Ala Pro Arg Ser Leu Gly Ile His Gly Phe Ala Gly Thr Ala Ala Pro
 210 215 220
 Gln Pro Cys Met Arg Ala Thr Val Gly Gly Leu Gly Val Leu Arg Ala
 225 230 235 240
 Ser Thr Gly Asp Ala Arg Pro Ala Thr
 245

<210> 21
 <211> 473
 <212> DNA
 <213> Artificial Sequence

002220"90272960

<220>

<223> Northern Blot Probe

<400> 21

ctgtggacgg	gggtggctat	gagatcctgc	cccgaagagc	agtactggga	tcctctgctg	60
ggtacctgca	tgtcctgcaa	aaccatttgc	aaccatcaga	gccagcgcac	ctgtgcagcc	120
ttctgcaggt	cactcagctg	ccgcaaggag	caaggcaagt	tctatgacca	tctcctgagg	180
gactgcatca	gctgtgcctc	catctgtgga	cagcacccta	agcaatgtgc	atacttctgt	240
gagaacaagc	tcaggagccc	agtgaacctt	ccaccagagc	tcaggagaca	gcggagtgga	300
gaagttgaaa	acaattcaga	caactcggga	aggtaccaag	gattggagca	cagaggctca	360
gaagcaagtc	cagctctccc	ggggctgaag	ctgagtgcag	atcaggtggc	cctgggtctac	420
agcacgctgg	ggctctgcct	gtgtgccgtc	ctctgctgct	tcctggtggc	ggt	473

<210> 22

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> ZC20061

<400> 22

ctgtggacag	gggtggctat	gagat	25
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<210> 23

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC20062

<400> 23

accgccacca	ggaagcacag	aggac	25
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<210> 24

<211> 256

<212> DNA

<213> Artificial Sequence

<220>

<223> Northern Blot probe

<400> 24

00220"90272960

tgcgattctc	tggaacctgtt	tggaactgag	cttaataatt	tctttggcag	ttttcgtgct	60
aatgtttttg	ctaaggaaga	taagctctga	accattaaag	gacgagttta	aaaacacagg	120
atcaggtctc	ctgggcatgg	ctaacattga	cctggaaaag	agcaggactg	gtgatgaaat	180
tattcttccg	agaggcctcg	agtacacggt	ggaagaatgc	acctgtgaag	actgcatcaa	240
gagcaaaccg	aaggtc					256

<210> 25

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC21065

<400> 25

tgcgattctc	tggaacctgtt	tg	22
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<210> 26

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC21067

<400> 26

gaccttcggt	ttgctcttga	tg	22
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<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC24200

<400> 27

acactggggg	tctgcctctg	20
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<210> 28

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

09627206-072700

<400> 28
gcgaagccgt gtatccc 17

<220>
<223> Oligonucleotide ZC24198

<210> 30
<211> 16
<212> DNA
<213> Artificial Sequence

<400> 30
gcacaagtgg ggtcgg 16

<220>
<223> Oligonucleotide ZC24271

<210> 32
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC24272

<400> 32
tagctgggag tggaaag 17

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC24495

<400> 33
tccaagcgtg accagttcag 20

<210> 34
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC24496

<400> 34
agttggcttc tccatccc 18

<210> 35
<211> 1090
<212> DNA
<213> Homo sapiens

<400> 35
taactctcct gaggggtgag ccaagccctg ccatgtagtg cacgcaggac atcaacaaac 60
acagataaca ggaaatgata cattccctgt ggtcacttat tctaaaggcc ccaaccttca 120
aagttcaagt agtgatatgg atgactccac agaaagggag cagtcacgcc ttacttcttg 180
ccttaagaaa agagaagaaa tgaaactgaa ggagtgtgtt tccatcctcc cacggaagga 240
aagcccctct gtccgatact ccaaagacgg aaagctgctg gctgcaacct tgctgctggc 300
actgctgtct tgctgcctca cgggtggtgtc tttctaccag gtggccgccc tgcaagggga 360
cctggccagc ctccgggcag agctgcaggg ccaccacgcg gagaagctgc cagcaggagc 420
aggagccccc aaggccggcc tggaggaagc tccagctgtc accgcgggac tgaaaatctt 480
tgaaccacca gctccaggag aaggcaactc cagtcagaac agcagaaata agcgtgccgt 540
tcagggtcca gaagaaacag tcaactcaaga ctgcttgcaa ctgattgcag acagtgaaac 600
accaactata caaaaaggat cttacacatt tgttccatgg cttctcagct ttaaaagggg 660
aagtgccta gaagaaaaag agaataaaat attggtcaaa gaaactggtt acttttttat 720
atatggtcag gttttatata ctgataagac ctacgccatg ggacatctaa ttcagaggaa 780

<210> 36
<211> 35
<212> DNA
<213> Artificial Sequence

<400> 36
cgcgcggttt aaacgccacc atggatgact ccaca 35

<220>
<223> Oligonucleotide

<210> 38
<211> 25
<212> DNA
<213> Artificial Sequence

<400> 38
tctggacgtc ctctgctgg tatag 25

<210>	39
<211>	25
<212>	DNA
<213>	Artificial Sequence

<223> Oligonucleotide ZC17252

ggtatggagc aaggggcaag ttggg

<213> Artificial Sequence

<223> Oligonucleotide ZC17156

gagtggcaac ttccagggcc aggagag

<213> Artificial Sequence

<223> Oligonucleotide ZC17157

cttttgctag cctcaaccct gactatc

<213> Homo sapiens

ggcacagcac	ggggcgatgg	gcgcgtttcg	ggccctgtgc	ggcctggcgc	tgtgtg'gcgc	60
gctcagcctg	ggtcagcgcc	ccaccggggg	tcccgggtgc	ggccctgggc	gcctcctgct	120
tgggacggga	acggacgcgc	gctgctgccg	ggttcacacg	acgcgctgct	gccgcgatta	180
cccgggcgag	gagtgtgttt	ccgagtggga	ctgcatgtgt	gtccagcctg	aattccactg	240
cggagaccct	tgtgacacga	cctgccggca	ccacccttgt	ccccaggcc	aggggggtaca	300
gtcccagggg	aaattcagtt	ttggcttcca	gtgtatcgac	tgtgcctcgg	ggaccttctc	360
cgggggccac	gaaggccact	gcaaaccctg	gacagactgc	accagttcg	ggtttctcac	420
tgtgttcctt	gggaacaaga	cccacaacgc	tgtgtgcgtc	ccagggtccc	cgccggcaga	480
gccgcttggg	tggctgaccg	tcgtcctcct	ggccgtggcc	gcctgcgtcc	tcctcctgac	540
ctcggccccag	cttggaactgc	acatctggca	gctgaggagt	cagtgcattg	ggccccgaga	600
gacccagctg	ctgctggagg	tgccgccgtc	gaccgaagac	gccagaagct	gccagttccc	660

cgaggaagag cggggcgagc gatcggcaga ggagaagggg cggctgggag acctgtgggt 720
 gtgagcctgg ctgtcctccg gggccaccga ccgcagccag cccctcccca ggagctcccc 780
 aggccgcagg gctctgcgtt ctgctctggg ccg 813

<210> 43

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC10.134

<400> 43

atcagcggaa ttcagatctt cagacaaaac tcacacatgc ccac 44

<210> 44

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC10135

<400> 44

ggcagtctct agatcattta cccggagaca gggag 35

<210> 45

<211> 768

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (7)...(759)

<223> Ig Fc sequence

<400> 45

ggatcc atg aag cac ctg tgg ttc ttc ctc ctg ctg gtg gcg gct ccc 48
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro
 1 5 10

aga tgg gtc ctg tcc gag ccc aga tct tca gac aaa act cac aca tgc 96
 Arg Trp Val Leu Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys
 15 20 25 30

cca ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc	144
Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu	
35 40 45	
ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag	192
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu	
50 55 60	
gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag	240
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys	
65 70 75	
ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag	288
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys	
80 85 90	
ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc	336
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu	
95 100 105 110	
acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag	384
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys	
115 120 125	
gtc tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa	432
Val Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys	
130 135 140	
gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc	480
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser	
145 150 155	
cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa	528
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys	
160 165 170	
ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag	576
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln	
175 180 185 190	
ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc	624
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly	
195 200 205	

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tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag 672
 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 210 215 220

cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac 720
 Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 225 230 235

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 His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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35

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15

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